Mouse Models of Brain Tumors and Their Applications in Preclinical Trials
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Abstract  Primary brain tumors, including gliomas and medulloblastomas, often represent the most devastating and difficult-to-treat tumors, and are thought to arise from glial cells and/or their precursors or the external granule cell layer, respectively. The majority of genetic alterations characteristic of the human brain tumors are thought to occur in genes encoding proteins involved in signal transduction or cell cycle regulation. Accurate recapitulation of these genetic alterations using genetically engineered mouse models allows for in vivo modeling of brain tumors with similar histopathology, etiology, and biology. These mouse models, in turn, increase our understanding of brain tumor initiation, formation, progression, and metastasis, providing an experimental system to discover novel therapeutic targets and test various therapeutic agents.

Of all cancer types, brain tumors probably represent the most devastating and difficult-to-treat cancer. Although enormous advances in treating other solid cancers, such as lung and breast cancers, highlighted the last decade, median survival for glioblastoma multiforme (GBM; the most common and aggressive primary brain tumor) stayed nearly the same over the last 50 years, averaging ~1 year (1). Regardless of advances in surgical and imaging techniques, we still face multiple problems when treating brain tumors, some because of extensive infiltration of tumors cells, their invasion into normal brain parenchyma or other sites, and resistance to standard radiation and chemotherapy. However, our paramount inability to successfully treat brain cancer mostly stems from the lack of understanding of the underlying brain tumor biology. Another problem common to diagnosing and thus treating the disease results from difficulties in classifying brain tumors often defined by histologic rather than molecular criteria. For example, histologically similar primary GBMs arising de novo and secondary GBMs progressing from low- to high-grade tumors will be classified and treated the same regardless of the vast disparity in molecular characteristics (2, 3). Although curing brain cancer might be in the distant future, we have gained some understanding of genetic and molecular characteristics of human brain tumors (4). Recent advances in laboratory techniques and successful development of brain tumor models faithfully recapitulating the human disease shed further light on necessity and sufficiency of genetic alterations for brain tumor initiation, progression, and maintenance; help identify relevant therapeutic targets; and provide an amenable field for testing novel therapeutic agents, translating into a better treatment for brain tumor patients.

Modeling Cancer for Drug Development

A multistep process of drug development is based on understanding the brain tumor characteristics by studying genomics, proteomics, genetics, and molecular epidemiology of the disease; preclinical studies is its making or breaking point (5). Preclinical studies culminate in patient clinical trials and translate to bedside upon success or are buried in dust otherwise, and, in turn, depend on our ability to accurately model the disease by using various research techniques and technologies. Approaches reiteratively used for cancer modeling during drug development are multidirectional and include a combination of in vitro cell culture experiments and in vivo use of animal models.

Cell culture. Cell culture experiments integral to drug development are commonly the first step in identifying therapeutic targets and addressing the effects of novel therapeutic agents (5). However, clinical trials have shown that these experiments often yield false-positive selections, because in vitro conditions do not recapitulate brain tumor environment, cause alterations in gene expression, acquisition of additional mutations, and differential selection resulting in clonal expansion of certain cell populations during culture times of primary normal or tumor cells. Primary tumor cultures rarely recapitulate cellular distribution within their tumor of origin; tumor cell lines cultured for decades certainly differ from tumors that gave rise to them (5–7). Although tumor-matrix interactions can be partially mimicked by providing cell cultures with matrix proteins and three-dimensional lattices, the full range of complex tumor-stromal interactions characterized by a combination of matrix proteins, serum and growth factors, hormones, and other substances is impossible to imitate. Likewise, many processes (tumor angiogenesis, invasiveness, and metastasis) dependent on the tumor-host interactions and essential for tumor initiation, formation, progression, and maintenance cannot be reproduced in vitro.
Animal models. In vivo modeling provides essential tumor-host interactions and is a more accurate means of modeling human cancer. Mouse models can be classified as xenograft tumor models or models of spontaneous tumor formation in genetically engineered mice (GEM), and help address issues of utmost importance in drug development: toxicity and in vivo antitumor effectiveness. Although the Food and Drug Administration does not require the latter before proceeding to clinical trials, in vivo modeling of drug efficacy is a gold standard required by a majority of pharmaceutical companies (5). Pharmacokinetic/pharmacodynamic models based on physiology and anatomic representation of bodily organs and drug biochemistry are likely to supplement in vivo modeling during future drug development (8).

Xenograft tumor models. Xenograft tumor formation frequently used for in vivo cancer modeling refers to implantation or injection of primary tumor cells or cell lines s.c. (under the skin) or orthotopically (into native tumor site) of immunosuppressed, immunodeﬁcient, or newborn immunonaive mice (9, 10). Xenograft tumors are characterized by synchrony and reproducibility of tumor formation, rapid tumor development, and high penetrance. Use of s.c. models allows for easy tumor visualization, making decisions of treatment initiation and drug application trivial. However, xenograft models lack stepwise genetic changes thought to occur during tumor progression; injected or implanted cells or cell lines can be serially transferred into immunocompromised or inbred mice (11). Immunosuppressed or immunocompromised mice do not show antitumor immune effects and can produce false positives during drug trials. Some of these problems were addressed by reducing culture times, implanting human tumor specimens with underlying native benign tumor stroma, and using immunonaive animals. However, xenograft tumor models do not faithfully recapitulate etiology, pathobiology, and biochemistry of human tumors they were derived from, making it hard to recognize drug effects and separate them from the experimentally induced artifacts (12–14).

Spontaneous tumors in GEMs. In principle, strains of mice forming spontaneous tumors due to mutations in the genes characteristic of a human malignancy are appealing due to predictability of the tumor-initiating lesion(s), immunocompetence, and tumor development at the appropriate site. Such spontaneous tumor formation recapitulates complex processes of ever-changing tumor genetic makeup, angiogenesis, tumor-host interactions, metastasis to distant sites, and can provide invaluable insights onto efficacy of single or multiple drug treatment on the preformed tumor (14). In addition, use of faithful GEMs is essential for modeling less common cancers due to limited patient population. However, at least in brain tumor modeling, the use of mouse models forming spontaneous tumors is complicated by poor reproducibility, low tumor penetrance, prolonged tumor formation latency, and a need for advanced in vivo imaging techniques. More complications arise from the fact that mutant alleles are often expressed or deleted from the whole animal or tissue, compared with human tumors that are thought to arise from a single mutant cell or a small mutant cell population. In this aspect, GEMs are more representative of human cancer predisposition syndromes rather than random tumorigenesis: presence of tumor-initiating mutation(s) in a large cell population may result in tumors characterized by decreased cell heterogeneity (14). In addition, promoters used for gene targeting might affect cell population different from the one that normally gives rise to corresponding human tumors. Even mouse tumors that phenocopy human tumors might be different genetically and molecularly, translating into a vastly different response to therapeutic agents.

GEM models are derived either by germline modification strategies or somatic cell gene transfer. Germline modification strategies refer to gain-of-function, conditional gain-of-function, loss-of-function, chromosome engineering, and RNA interference (15). Gain-of-function models involve creating transgenic animals characterized by allele expression related to the normal gene, ubiquitous/constitutive or tissue/stage-specific, or the knock-in animals, in which endogenous genetic segment is replaced by an exogenous or mutant counterpart. The latter can result in embryonic lethality and spontaneous tumor formation at ectopic sites. Conditional gain-of-function models circumvent the problem by allowing oncogene expression activation by drug treatment (4-hydroxytamoxifen or tetracycline) or recombination (Cre/Flip induced or spontaneous; ref. 15). Loss-of-function approaches involve replacement of endogenous genetic segments with terminating elements (positive selection markers) or creating conditional knockout mice containing floxed/flirted alleles excised upon Cre/Flip-mediated recombination (15). Chromosome engineering allows modeling chromosomal translocations, deletions, and inversions by placing recombination target sequences in various orientations and/or at different chromosomal positions. By contrast, RNA interference strategies are based on sequence-specific mRNA silencing by short hairpin RNAs after the gene product has already been transcribed (15).

Somatic cell gene transfer differs from germline modification strategies because it is not heritable and presents a modified gene product to targeted cell population rather than to the whole host. Somatic cells genetically modified by viral vectors to become cancerous can pass on acquired mutation(s) to daughter cells. Most commonly used single-stranded RNA viruses are murine or avian. Although murine retroviruses can infect all previously uninfected cells upon a single round of replication, additional viral receptor expression is essential for infection with an avian retrovirus. Use of avian retroviruses has been successfully applied in the RCAS/tv-a system, which uses replication-deficient ALV-spike acceptor retroviral vector carrying an oncogene and mice genetically engineered to express tv-a receptor that binds RCAS in a certain cell population (16, 17). Both types of retroviruses can be delivered to cultured cells and secondarily transferred into mice (e.g., by primary tv-a cell infection and reinjection into the autologous or immunocompromised host), or used for direct in vivo infections (e.g., by i.p. or target-tissue injection of cell-free supernatant, or producer cell injection into the target tissue after birth). Nondividing cells can be infected using Moloney murine leukemia virus (MMLV)–based lentiviral systems, subject to compatibility between targeted cell type and vector envelope (18). Widely used viral transfer models include transplantation of fetal cells infected with engineered retroviruses, direct in vivo infection with MMLV-based systems, or direct gene transfer in vivo using RCAS vectors. Although MMLV-based lentiviral...
systems allow infecting nondividing cells, RCAS/tv-a system is more specific and allows for lineage tracing from a limited cell-of-origin population of a certain differentiation stage, use of oncogene combinations, addressing the effects of a specific oncogene within the tumor environment, and use of bicistronic vectors encoding an oncogene and a modifying or a labeling gene (e.g., another oncogene, fluorescent reporter gene; refs. 16–18).

**Brain Tumors: Gliomas and Medulloblastomas**

**Classification and histology.** Normal brain is composed of a variety of cell types, including neurons, glia (astrocytes, oligodendrocytes, microglia, and ependymal cells), vascular epithelium, and meningeal cells. Primary brain tumors can be classified into gliomas, the most common adult brain tumors occurring in the brain parenchyma above the tentorium, and medulloblastomas, child or young adult cerebellar tumors occurring below the tentorium (9). Intracranial tumors arising from brain meninges (meningiomas) and tumor metastases from systemic cancers (lung, breast, colon) are not considered primary brain tumors and will not be discussed.

Depending on morphologic and histologic similarities to the normal cells, gliomas can be classified as astrocytic, oligodendrocytic, or mixed, and are proposed to arise from the respective cell type (9, 19). The WHO classification divides astrocytic tumors into grades 1 to 4, grade 4 GBM being the most aggressive and malignant primary glioma. Astrocytic tumors (including GBMs) are composed of glial fibrillary acidic protein (GFAP)—expressing cells with fibrillary cytoplasm and angular nuclei, whereas GFAP-negative oligodendroglial tumors present uniform cells with rounded nuclei. GBM features include microvascular proliferation, nuclear atypia, presence of giant cells, and pseudopalisading necrosis. Histologically indistinguishable but molecularly/genetically distinct primary and secondary GBMs develop as primary de novo tumors or progress from the diffuse grade 2 to anaplastic grade 3 astrocytomas and to secondary GBMs. Similar WHO classification subdivides oligodendrogliomas into grade 2 low-grade and grade 3 anaplastic oligodendrogliomas. Although patients with low-grade gliomas survive for 10 to 15 years, patients with grade 3 astrocytomas survive for only 2 to 3 years; the mean survival for patients with a GBM is ~1 year (1, 19).

Medulloblastomas, “blue-cell tumors” composed of small cells with little cytoplasm, are locally invasive and express synaptophysin and NeuN. These cerebellar tumors are classified as desmoplastic, if they contain large-cytoplasmic cell islands in the field of more typical medulloblastomas cells, or as large cell, if they contain large pleomorphic cells. Medulloblastomas show good prognosis with a 65% to 85% cure rate and a high possibility of complete resection; yet, CSF tumor cell spreading and severe neuroaxis irradiation effects still pose a problem (9, 19).

**Initial mouse brain tumor models.** Initial spontaneous tumor models relied on direct or transplacental exposure to mutagenic DNA alkylating agents (e.g., nitrosoureas) causing point mutations (20). Resulting brain tumors contained multiple random genetic alterations and were histologically similar to human brain tumors, but tumor-initiating mutations and cell(s) of origin were obscured. Xenograft or allograft tumor models developed at the same time are still extensively used for testing novel therapeutic agents (10).

**Genetic abnormalities in brain tumors.** Frequently occurring somatic mutations and pathway abnormalities potentially implicated in human glioma initiation/progression have been identified in recent years. Most of them occur in genes implicated in signal transduction or cell cycle control, e.g., growth factor overexpression, gain-of-function mutations in receptor tyrosine kinases, and tumor suppressor loss (9). Genetic aberrations accumulate as tumors progress in grade and are sometimes indicative of the tumor formation process: primary GBMs normally contain epidermal growth factor receptor amplification, mutations or deletions of PTEN, and deletions of the ink4a/arf locus; secondary GBMs contain p53 mutations. Genetic alterations in medulloblastomas and their importance in tumor initiation/progression are less well explored. However, in-depth understanding of Shh-dependent subset of medulloblastomas, which accounts for 20% of the human disease, represents one of the success stories in using animal models to study rare childhood cancers.

Activation of phosphatidylinositol 3-kinase (PI3K)/Akt, RAS/mitogen-activated protein kinase, phospholipase C/protein kinase C signal transduction pathways affecting cell proliferation, differentiation, apoptosis, and protein translation in human gliomas is frequently achieved by growth factor overexpression [e.g., fibroblast growth factor, ciliary neurotrophic factor, epidermal growth factor (EGF), platelet-derived growth factor (PDGF)] or activating mutations in corresponding receptors (Fig. 1A; ref. 9). PTEN, tumor suppressor negatively regulating Akt activity and frequently lost or mutated in primary GBMs, implicates Akt signaling in tumor formation. Deletion of the ink4a/arf locus in human gliomas causes cell cycle control disruption due to involvement of its gene products in two major cell cycle regulatory pathways: Rb and p53 (Fig. 1A). CDK4 amplifications are present in a small number of GBMs, Rb is affected in a third of anaplastic gliomas, and both p53 mutations and ink4a/arf loss occur in the majority of anaplastic and a third of low-grade gliomas. Mutations of several components of the same pathway are rare in gliomas, but frequent presence of p53 mutations with CDK4 overexpression or Rb loss point to the importance of both pathways in gliomagenesis (9). Medulloblastomas, on the other hand, are often characterized by loss of heterozygosity of an unidentified tumor suppressor gene located on 17p distal to p53. An aggressive subset of medulloblastomas is characterized by Myc amplification/overexpression; some medulloblastomas show germline mutations in Ptch (receptor for Shh) and deregulation of Shh signaling that stimulates precursor cell proliferation (Fig. 1B). In addition, Notch signaling is essential for growth and survival of Shh-induced medulloblastomas (Fig. 1B; ref. 21).

**GEM brain tumor models.** Identification of genetic and molecular characteristics of human brain tumors raised questions of their necessity and sufficiency for different stages of tumorigenesis. Somatic cell gene transfer and germline modifications allow demonstrating causality: advances in mouse genetic techniques and understanding developmental biology make it possible to target oncogenic mutations to cells of various differentiation stages of the neural lineage tree, defining two variables in brain tumorigenesis—initiating mutation and tumor cell(s) of origin. Conditional mouse models and somatic gene transfer additionally allow time-dependent control over mutant allele expression and contribution of several oncogenes to brain tumor initiation.
Early mouse models of astrocytic tumors based on experiments in other species involved transgenic expression of v-src (v-src kinase mediating signaling from PDGF, EGF, and PI3K) from the GFAP promoter and resulted in astrocytomas in 15% to 50% of mice, depending on transgene copy number (Table 1; ref. 22). Although Ras mutations are uncommon in human gliomas, activation of Ras signaling often occurs as a result of upstream factors and can activate Raf/MEK/Erk, Rac/Jnk/Ink, MKK/p38, phospholipase C/protein kinase C, and PI3K/Akt pathways (Fig. 1A; ref. 23). Transgenic mice expressing V12H-Ras from GFAP promoter developed astrocytomas in 95% cases by 4 to 6 months; mice homozygous and heterozygous for Ras pathways (Fig. 1A; ref. 23). Transgenic mice expressing MKK/p38, phospholipase C/protein kinase C, and PI3K/Akt signaling showed 50% survival at 3 and 12 weeks, respectively, implicating Ras in dose-dependent tumor initiation (Table 1; ref. 24). Molecular analysis of these tumors showed overexpression of CDK4, MDM2, and EGFR receptor (EGFR), decreased levels of Ink4a/arf and PTEN, and activation of signaling pathways stimulated by the active H-Ras. However, majority of Ras mutations in human gliomas are found in K-Ras and not H-Ras, and knockout K-Ras, N-Ras, and H-Ras mice show different phenotypes. Thus, specific roles of Ras isoforms in gliomagenesis are unknown (25).

Initially, oligodendrogliomas were found in ~10% of Arf null mice (Table 1). Subsequent developments using RCAS/tv-a system showed that PDGF signaling is sufficient for tumor formation (Table 1; refs. 9, 26). Gene transfer into nestin-expressing progenitors resulted in low-grade oligodendroglioma formation in ~60% mice by 12 weeks, whereas infection of GFAP-expressing cells resulted in oligodendrogial and mixed gliomas in ~40% of mice. Inka4a/arf loss increased PDGF-induced tumor incidence and malignancy, and PDGF signaling showed dosage effect during gliomagenesis. PDGF 5’ untranslated region removal resulted in elevated PDGF expression and 97% incidence of high-grade oligodendrogliomas upon gene transfer into nestin-expressing progenitors. Although PDGF transiently activated PI3K, Ras, phospholipase Cγ, and signal transducers and activators of transcription, resulting oligodendrogliomas did not show elevated activity of PI3K/Akt or Ras/mitogen-activated protein kinase pathways (9, 26). Rho deregulation by p190RhoGAP (negative Rho regulator involved in oligodendrocyte differentiation) contributed to PDGF-induced gliomagenesis (26). EGFR abnormality frequent in human oligodendrogliomas resulted in a model expressing v-erbB (activated EGF) from the S100β promoter active in both progenitors and differentiated astrocytes, showing 63% low-grade oligodendroglioma incidence at 1 year, and tumor grade, penetrance, and latency increased by additional p53 or Inka4a/arf loss (Table 1; ref. 27). Crossing GFAP-V12H-Ras mice to GFAP-EGFRvIII transgenics with the mutation most common in malignant gliomas resulted in aggressive oligodendrogial or mixed gliomas in double but not single transgenics (Table 1; ref. 28).

All human GBMs present elevated Ras activity; increased Akt activity unrelated to activating Akt mutations is present in 75% of them (Fig. 1A; ref. 9). GBM modeling using RCAS/tv-a and constitutive expression of K-Ras and Akt in nestin-expressing progenitors implicated these genetic pathways as causal in GBM formation, resulting in 26% tumor incidence at 12 weeks (Table 1). Single or combined expression of activated K-Ras or Akt in GFAP-positive differentiated cells did not result in GBM formation using RCAS/tv-a, whereas high levels of H-Ras were sufficient to cause GBMs in GFAP-V12H-Ras mice (9, 26). RCAS/tv-a and Cre/loxP modeling with PTEN loss in nestin-positive progenitors implicated combined PTEN loss and Ras activation in GBM formation comparable with K-Ras and Akt (26). Resulting GBMs exhibited similar histology, incidence, latency, and gene expression, proving that oncogenic effects of PTEN loss are mediated by increased Akt activity. GBM modeling by double heterozygous p53/Nf1 loss exhibited variable numbers of secondary GBMs depending on loss of heterozygosity (Table 1; ref. 29). Conditional astrocyte-specific Nf1-knockout mice did not result in glioma formation, implying that GBMs either did not arise in astrocytes or depended on loss of both tumor suppressors. MMLV-based PDGF mouse model showed 40% tumor incidence, the majority being histologically similar to human GBMs and some resembling oligodendrogliomas or neuroectodermal tumors, potentially due to high infection and insertional mutagenesis rates or promiscuity of MMLV-based vectors, making it hard to identify tumor cells of origin (Table 1; ref. 18).

Shh pathway activation or equivalent loss of Ptch combined with Akt activation or cell cycle arrest disruption allows for medulloblastoma modeling (Fig. 1B; Table 1; refs. 9, 30). Mice heterozygous for Ptch showed 15% tumor incidence at 1 year, increasing to 95% at 12 weeks upon p53 loss (Table 1; refs. 9, 30). MMLV-based and RCAS/tv-a models using viral vectors encoding Shh showed low tumor incidence; additional overexpression of c-Myc using RCAS/tv-a targeting nestin-positive progenitors enhanced tumor incidence to 30%. Akt activation or IGF2 overexpression in the latter mouse model enhanced tumor incidence and shortened tumor latency (Table 1; ref. 31). Although p53 and Rb are rarely mutated in human medulloblastomas, their combined loss in granule cell layer precursors resulted in 100% tumor incidence and histologic similarities to human medulloblastomas (Table 1; ref. 32). A p53-null mouse model with additional loss of poly(ADP-ribose)polymerase-1 (polymerase implicated in DNA repair) showed 50% tumor incidence with signaling abnormalities in the Shh pathway. Lig4 (DNA repair enzyme) loss in the p53-null mice resulted in medulloblastoma formation as well (9). Recently developed GEMs overexpressing Smo in cerebellar granule layer precursor cells (ND2:SmoA1) showed 48% medulloblastoma incidence, characterized by high levels of Gl1, N-myc, Notch2, and HES5 (Table 1; ref. 34).

**In vivo Imaging Technologies**

Imaging modalities offer the possibility of adding in vivo monitoring of live animals for diagnostic purposes of tumor identification, observing tumor progression and longitudinal effects of drug action, each mouse being its own control. Magnetic resonance imaging, the representative image of which is shown in Fig. 2, can be used to quantify tumor volumes, evaluate tumor vasculature, and study tumor physiology and biochemistry of drug response in vivo (9, 34). In contrast, bioluminescence allows molecular imaging and monitoring of biological changes in cells and organisms using luciferase-expressing transgenic mice and sensitive photon detectors to collect light transmitted through mammalian tissues with a high signal-to-noise ratio and without the use of contrast-enhancing agents (Figs. 2 and 3; ref. 35).
Preclinical Trials in GEMs

GEMs closely recapitulate the human disease and are used to predict human response to a therapy, treatment or radiation schedule. Yet, GEM-tested pathway inhibitors often affect pathways used for brain tumor induction, based on the frequently failing assumption of continued need of the initiating lesion to maintain tumorigenesis (Figs. 1 and 3). However, during tumor progression, cancer cells may acquire additional mutations to become independent of the cancer-initiating lesions or resistant to a therapeutic agent, the former circumvented by inducible GEMs, which allow testing oncogene requirement for tumor maintenance and progression. In addition, human brain tumors are thought to result from accumulation of several genetic alterations, implying that targeting a single oncogenic pathway is likely to be insufficient for brain tumor treatment.

Current approaches in brain tumor management. Glioma and medulloblastoma treatments normally include tumor resection, histologic examination, radiation therapy, and chemotherapy. The most common chemotherapeutic agents used for glioma treatment are DNA alkylating cytotoxic drugs such as carmustine [1,3-bis(2-chloroethyl)-1-nitrosourea]; a triple combination of procarbazine, cisplatin, and vincristine; or the recently developed temozolomide, etoposide, or lomustine, whereas those used for medulloblastoma treatment are cisplatin, cyclophosphamide, or vincristine. Due to the time of incidence and its nature, medulloblastoma cure rate is 85% for children with nondisseminated tumors and 65% to 70% in high-risk patients (36). However, drugs listed above present serious side effects and eventually fail as patients develop resistance, whereas radiation and chemotherapy adversely affect neurocognitive and physical development (26, 37). Thus, although traditional brain tumor therapeutics relied on nonspecific cytotoxic agents, preventing cell proliferation and resulting in cell death due to DNA damage or disrupted cell division, current therapeutic agents are developed to avoid normal cell toxicity and target tumor...
cell-specific antigens and cell alterations responsible for growth, proliferation, invasion, and metastasis.

**Therapeutic agents targeting signal transduction.** Signaling abnormalities downstream of EGFR/PDGF receptor (PDGFR) and Ras/Akt pathways common in gliomas are frequently targeted with EGFR, PDGFR, mammalian target of rapamycin (mTOR), Akt, and Ras inhibitors (Fig. 1A; refs. 9, 26). EGFR inhibitors tested in vitro glioma cell lines and xenograft mouse tumor models during preclinical trials and currently in phase I/II clinical trials include Tarceva (erlotinib, OSI-774), Iressa (gefitinib, ZD1839), and an EGFR/vascular endothelial growth factor receptor 2 tyrosine kinase inhibitor AEE788 (38–40).

GEMs useful for addressing roles of EGFR signaling in tumor maintenance and progression or testing novel inhibitors include GFAP-V12H-Ras, GFAP-EGFRvIII, and S100β-v-erbB mouse models (Table 1; refs. 27, 28).

PDGFR signaling abnormalities are present in histologically unlike high-grade gliomas. Selective PDGFR/vascular endothelial growth factor receptor inhibitor PTK787/ZK222584 effective in converting high-grade oligodendrogliomas to low-grade tumors and inhibiting tumor proliferation without disrupting tumor vasculature in RCAS/tv-a GEM of PDGF-induced gliomagenesis is now in preclinical trials (Fig. 1; ref. 41).

Other potentially useful PDGFR inhibitors tested in in vitro and in vivo xenograft models but not in GEMs include Gleevec (imatinib mesylate, STI-571), a PDGFR/c-kit/bcr-abl tyrosine kinase inhibitor.

**Figure 1 continued.** B, activation of Shh and Notch pathways typical for human and GEM medulloblastomas. Green box areas, molecular inhibitors of various pathway components. Their therapeutic targets are indicated adjacently.
kinase inhibitor successful in treating chronic myelogenous leukemia and gastrointestinal stromal tumors, SU6668, PDGFRβ/vascular endothelial growth factor receptor 2/fibroblast growth factor receptor 1 tyrosine kinase inhibitor, and CP-673,451, PDGFRβ phosphorylation inhibitor (26, 42, 43).

Deregulated PI3K/Akt signaling proposed to account for tumor cell growth and resistance to radiation/chemotherapy is frequent in many cancers. Perifosine (orally administered compound causing Akt inhibition), now in preclinical trials, is cytotoxic to human tumor cell lines, causes dose-dependent growth inhibition, and induces G1-G2 cell cycle arrest in Ras+Akt-driven mouse progenitors. Perifosine synergizes with temozolomide (alkylating agent) in vitro cultures of mouse progenitors and in RCAS/tv-a GEM of PDGF-induced tumorigenesis (Fig. 1; ref. 44). Other PI3K/Akt signaling inhibitors effective in vitro and in vivo xenograft models but yet to be tested using GEMs include PWT-458 (pegylated-17-hydroxysteroidomin, induces loss of Akt phosphorylation, and synergizes with rapamycin), LY294002 (reverses PI3K-induced radiation resistance), and protein kinase Cβ-selective inhibitor enzastaurin (LY317615.HCl, suppresses Akt signaling; refs. 45–47).

Akt activation mainly targets mTOR, which can be inhibited by rapamycin (sirolimus), CCI-779 (temsirolimus), and RAD001 (everolimus; Figs. 1 and 3). Tumor cells of brain and other cancers show differential sensitivity to mTOR inhibitors. CCI-779 induces tumor cell death in a subset of cells at 48 hours of drug treatment using RCAS/tv-a GEM of K-Ras+Akt-induced GBM formation, endowing surviving tumor cells with histologic characteristics of oligodendroglial tumors with low Akt activity after 7-day treatment (26, 48). Thus, astrocytic GBM characteristics seem dependent on mTOR signaling. Use of mTOR inhibitors might be beneficial for patients with tumors characterized by PTEN loss, which has been shown equivalent to Akt activation by the RCAS/tv-a GEM.

<table>
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<th>Tumor classification</th>
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<td>SmoA1</td>
<td>Gain</td>
<td>ND2</td>
<td>33</td>
</tr>
<tr>
<td></td>
<td>Shh + Akt or IGF2</td>
<td>Gain</td>
<td>Nestin</td>
<td>31</td>
</tr>
</tbody>
</table>

NOTE: Tumor cells of origin are unknown in the knockout GEMs; promoters used for somatic cell gene transfer or limiting transgene expression are listed and correspond to glioneuronal progenitor cells (nestin, S100βi), differentiated astrocytes (GFAP), or the external granule layer progenitor cells (ND2).
prenyltransferases adding geranylgeranyl or farnesyl groups at COOH-terminal Ras CAAX sequences. Ras activity elevated in human GBMs and frequent in lower-grade astrocytomas can be therapeutically targeted by small-molecule inhibitors acting on downstream effectors, or farnesyltransferase inhibitors and S-trans-farnesylthiosalicylic acid preventing Ras interactions with downstream components (Fig. 1). There is no published data describing the effects of these therapeutic agents.
in GEMs, but some look promising by in vitro experiments, in vivo xenograft models, and effective treatments of other cancers. Small-molecule inhibitors include BAY43-9006 ( Raf small-molecule inhibitor ) and PD184352/C1-1040 (Mek small-molecule inhibitor); farnesyltransferase inhibitors include Zarnestra (tipifarnib, R115777), evaluated in phase I clinical trials for gliomas; Sarasar (lonafarnib, SCH66336) in clinical trials for other types of cancer; and prenylation inhibitors L-778,123 and BMS-214662 (26, 49). GEMs that form Ras-driven gliomas (e.g., GFAP-V12H-Ras mice) could be useful for these preclinical trials (Table 1; ref. 28).

Use of single agents is rarely sufficient to halt tumor progression due to independence from the tumor-initiating mutation, cellular heterogeneity within tumors, and a variety of signaling patterns. Clinical and preclinical studies using drug combinations underscore the necessity of multilevel targeting, exhibiting better results in combination rather than single-agent use. For example, human GBM xenografts in athymic mice were better inhibited by a combination of EGFR/vascular endothelial growth factor receptor 2 tyrosine kinase inhibitor AEE788 and mTOR inhibitor RAD001, producing higher cell cycle arrest rates and reduced in vitro proliferation (50). Similarly, PDGF-induced gliomas in RCAS/TV-a GEMs showed in vitro and in vivo synergy between Akt inhibitor perifosmine and alkylating agent temozolomide.

Some therapeutic glioma agents might be useful for medulloblastoma treatment due to its frequent overexpression of EGFR and/or its ligands, Akt, PDGFR, and c-kit, which can be targeted by tyrosine kinase small-molecule inhibitor lapatinib (GW572016), CCI-779, and Gleevec (imatinib mesylate, STI-571; Fig. 1; refs. 26, 52). Some of these agents were tested in vitro and in vivo xenograft tumors, but not in GEMs. Therapeutic agents tailored to medulloblastoma-specific signaling abnormalities include Shh-Gli, Notch, and γ-secretase inhibitors (Fig. 1B). Shh-Gli signaling inhibitors tested in Ptc1(+/-); p53(−/−) GEMs include cyclopamine (alkaloid found in Veratum californiicum) and HhAntag, both impairing activity of Smoothened (Fig. 1; refs. 52, 53). Cyclopamine administration resulted in reduced tumor burden, lower proliferation rates, and smaller numbers of Ptc1-expressing cells, whereas HhAntag caused inhibition of cell proliferation, extensive cell death, and tumor eradication at high doses (53, 54). Interestingly, p53 loss did not make Shh-dependent tumors resistant to pathway inhibitors. Notch and γ-secretase inhibitor DAPT was shown to be effective in in vitro and in vivo xenograft tumors, but not in Shh-driven GEMs tumors (Fig. 1; ref. 33).

Non–signal transduction-based therapeutic agents. A number of other strategies yet to be tested in GEM models of brain tumorigenesis include histone deacetylase inhibitors (54), immune modulation (55, 56), angiogenic therapy (58), monoclonal antibodies (59, 60), small interfering RNA approaches (52), and differentiation therapy (61). These therapies are interesting for their flexibility, which allows tailoring treatment to specific tumors and their environment by choosing antigens, antibodies, appropriate toxin or isotope conjugates, or administration methods.

Conclusions

Our increasing knowledge of underlying brain tumor biology suggests that brain tumor therapeutics is in its infancy—we still lack detailed understanding of mechanisms of drug actions, optimal concentrations, treatment schedules, and treatment course. Regardless of technological developments in the operating rooms, brain tumor patients still face a dim prognosis. Using in vitro systems and in vivo xenograft brain tumor modeling provides a quick and efficient way of testing novel therapeutic agents and targets, knowledge from which can be translated and tested in more sophisticated GEMs that faithfully recapitulate human brain tumors and will likely result in high-quality clinical trials with satisfactory treatment outcomes and reduced drug toxicities. Additional use of GEMs to establish causal links between the presence of various genetic alterations and brain tumor initiation or determining their necessity for tumor maintenance and/or progression provides us with a glimpse into other important aspects of brain tumor biology. Developing GEMs with multiple genetic abnormalities typical for human brain tumors and advancing imaging technologies will allow testing drug combinations, high-resolution mapping with an easy readout for the therapeutic efficacy, and longitudinal drug monitoring during preclinical trials. Thus, although curing brain tumors might still be in the distant future, we are advancing further in development of various therapies targeting different aspects of the enemy we have long sought to defeat.

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